



SEQUENCE LISTING

<110> DAI, KEN SHUO

<120> HUMAN ARL-RELATED GENE VARIANTS ASSOCIATED WITH CANCER

<130> U014798-3

<140> 10/653,681

<141> 2003-09-02

<160> 4

<170> PatentIn version 3.2

<210> 1

<211> 1090

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

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<221> CDS

<222> (70)..(333)

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Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro  
1 5 10

att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa 159  
Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu  
15 20 25 30

gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc 207  
Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala  
35 40 45

tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag 255  
Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys  
50 55 60

atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag 303  
Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys  
65 70 75

ttg tgg ccc act tcc aga tcg aga agc tct tgaacaaacc tggactgaaa 353  
Leu Trp Pro Thr Ser Arg Ser Arg Ser Ser  
80 85

tataaaccag tgactaacca ggttgagtgt cacccataacc tcacgcagga gaaactgatc 413

cagtaactgcc actccaagggg catcacgggtt acggcctaca gccccctggg ctctccggat 473

agacaccttggg ccaagccaga agacccttcc ctgctggagg atcccaagat taaggagatt 533

gctgcaaagc acaaaaaaaaac	cgcagcccag gttctgatcc	gttccatat ccagaggaat	593
gtgattgtca tccccaaagtc	tgtgacaccca gcacgcattg	ttgagaacat tcaggtctt	653
gactttaat tgagtgtatga	ggagatggca accatactca	gcttcaacag aaactggagg	713
gcctgtaacg tggtgcaatc	ctctcatttga agaactatc	ccttcgatgc agaatattga	773
ggttgaatct cctggtgaga	ttatacagga gattctttt	cttcgctgaa gtgtgactac	833
ctccactcat gtcccatttt	agccaagctt atttaagatc	acagtgaact tagtcctgtt	893
atagacgaga atcgaggtgc	tgttttagac atttatttct	gtatgttcaa ctaggatcag	953
aatatcacag aaaagcatgg	cttgaataag gaaatgacaa	tttttccac ttatctgatc	1013
agaacaaaatg tttattaagc	atcagaaaact ctgccaacac	tgaggatgta aagatcaata	1073
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<212> PRT

<213> ARTIFICIAL SEQUENCE

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<223> PEPTIDE ENCODED BY VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

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Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro Ile Val			
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Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val		
20	25	30

Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val		
35	40	45

Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln		
50	55	60

Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp			
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Pro Thr Ser Arg Ser Arg Ser Ser	
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<210> 3

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<212> DNA

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<223> VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

<220>

<221> CDS

<222> (70)..(804)

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1 5 10	
att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu	159
15 20 25 30	
gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala	207
35 40 45	
tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys	255
50 55 60	
atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys	303
65 70 75	
ttg tgg ccc act ttc ttt gag aga ccc ctt gtg agg aaa gcc ttt gag Leu Trp Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu	351
80 85 90	
aag acc ctc aag gac ctg aag ctg agc tat ctg gac gtc tat ctt att Lys Thr Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile	399
95 100 105 110	
cac tgg cca cag gga ttc aag tct ggg gat gac ctt ttc ccc aaa gat His Trp Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp	447
115 120 125	
gat aaa ggt aat gcc atc ggt gga aaa gca acg ttc ttg gat gcc tgg Asp Lys Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp	495
130 135 140	
gag gcc atg gag gag ctg gtg gat gag ggg ctg gtg aaa gcc ctt ggg Glu Ala Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly	543
145 150 155	
gtc tcc aat ttc agc cac ttc cag atc gag aag ctc ttg aac aaa cct Val Ser Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro	591
160 165 170	
gga ctg aaa tat aaa cca gtg act aac cag gtt gag tgt cac cca tac Gly Leu Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr	639
175 180 185 190	

ctc acg cag gag aaa ctg atc cag tac tgc cac tcc aag ggc atc acc	687
Leu Thr Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr	
195 200 205	
gtt acg gcc tac agc ccc ctg ggc tct ccg gat aga cct tgg gcc aag	735
Val Thr Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys	
210 215 220	
cca gaa gac cct tcc ctg ctg gag gat ccc aag att aag gag att gct	783
Pro Glu Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala	
225 230 235	
gca aag cac tcc cca agt ctg tgacaccaggc acgcattgtt gagaacattc	834
Ala Lys His Ser Pro Ser Leu	
240 245	
aggtcttga cttaaattt agtgatgagg agatggcaac catactcagc ttcaacagaa	894
actggagggc ctgtaacgtg ttgcaatcct ctcatttgg a gactatccc ttcatgcag	954
aatattgagg ttgaatctcc tggtagatt atacaggaga ttctctttct tcgctgaagt	1014
gtgactacct ccactcatgt cccatTTAG ccaagcttat ttaagatcac agtgaactta	1074
gtcctgttat agacgagaat cgaggtgctg ttttagacat ttattctgt atgttcaact	1134
aggatcagaa tatcacagaa aagcatggct tgaataagga aatgacaatt tttccactt	1194
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gatcaataaa aaaaataata atcat	1279

<210> 4  
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<212> PRT  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> PEPTIDE ENCODED BY VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

<400> 4

Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro Ile Val  
1 5 10 15

Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val  
20 25 30

Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val  
35 40 45

Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln  
50 55 60

Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp

65

70

75

80

Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu Lys Thr  
85 90 95

Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile His Trp  
100 105 110

Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp Asp Lys  
115 120 125

Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp Glu Ala  
130 135 140

Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly Val Ser  
145 150 155 160

Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro Gly Leu  
165 170 175

Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr Leu Thr  
180 185 190

Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr Val Thr  
195 200 205

Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys Pro Glu  
210 215 220

Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala Ala Lys  
225 230 235 240

His Ser Pro Ser Leu  
245